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# Outline of Microarray Chip Technology

approach

cdNA Targets

Cy3

Cy5

Increased Expression



|   |   |   |   |   |   |   |   |   |    |    |    |
|---|---|---|---|---|---|---|---|---|----|----|----|
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |
| A |   |   |   |   |   |   |   |   |    |    |    |
| B |   |   |   |   |   |   |   |   |    |    |    |
| C |   |   |   |   |   |   |   |   |    |    |    |
| D |   |   |   |   |   |   |   |   |    |    |    |
| E |   |   |   |   |   |   |   |   |    |    |    |
| F |   |   |   |   |   |   |   |   |    |    |    |
| G |   |   |   |   |   |   |   |   |    |    |    |
| H |   |   |   |   |   |   |   |   |    |    |    |

|   |   |   |   |   |   |   |   |   |    |    |    |
|---|---|---|---|---|---|---|---|---|----|----|----|
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |
| A |   |   |   |   |   |   |   |   |    |    |    |
| B |   |   |   |   |   |   |   |   |    |    |    |
| C |   |   |   |   |   |   |   |   |    |    |    |
| D |   |   |   |   |   |   |   |   |    |    |    |
| E |   |   |   |   |   |   |   |   |    |    |    |
| F |   |   |   |   |   |   |   |   |    |    |    |
| G |   |   |   |   |   |   |   |   |    |    |    |
| H |   |   |   |   |   |   |   |   |    |    |    |

FIG. 1

# General protocol for *in-vivo* whole gene CD8 T cell priming

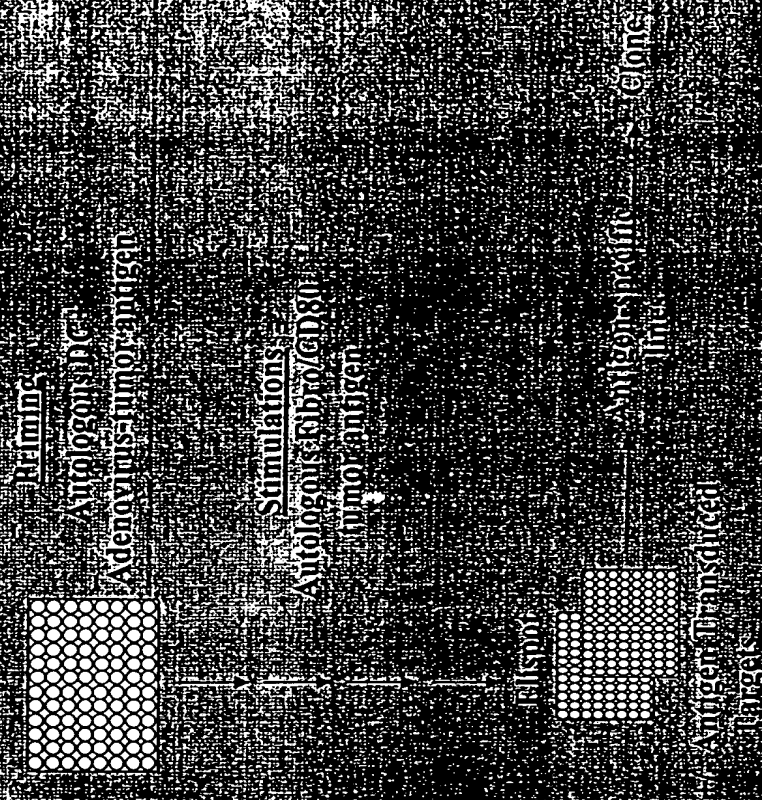


FIG. 2

# General protocol for *in-vitro* whole gene CD4 T cell priming

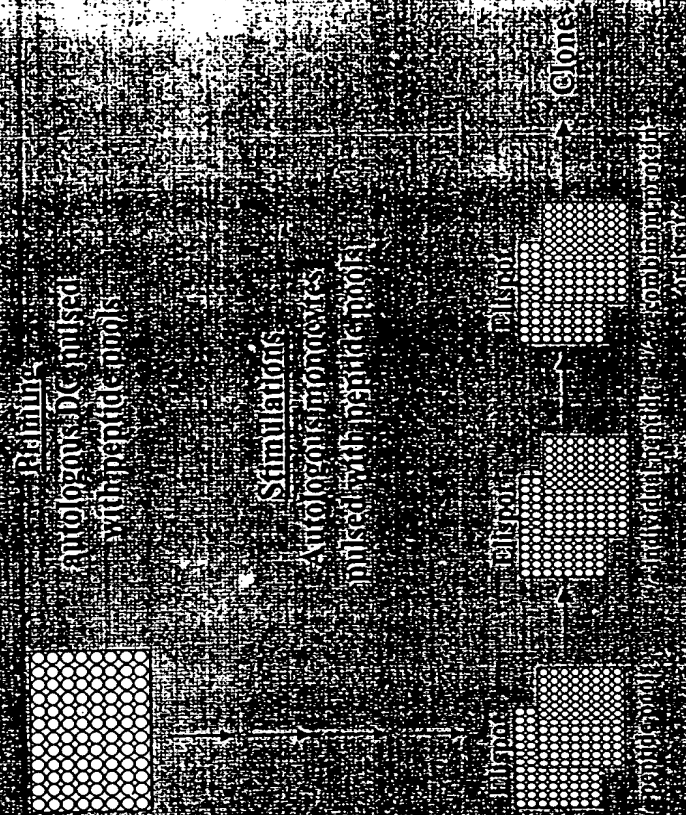


FIG. 3

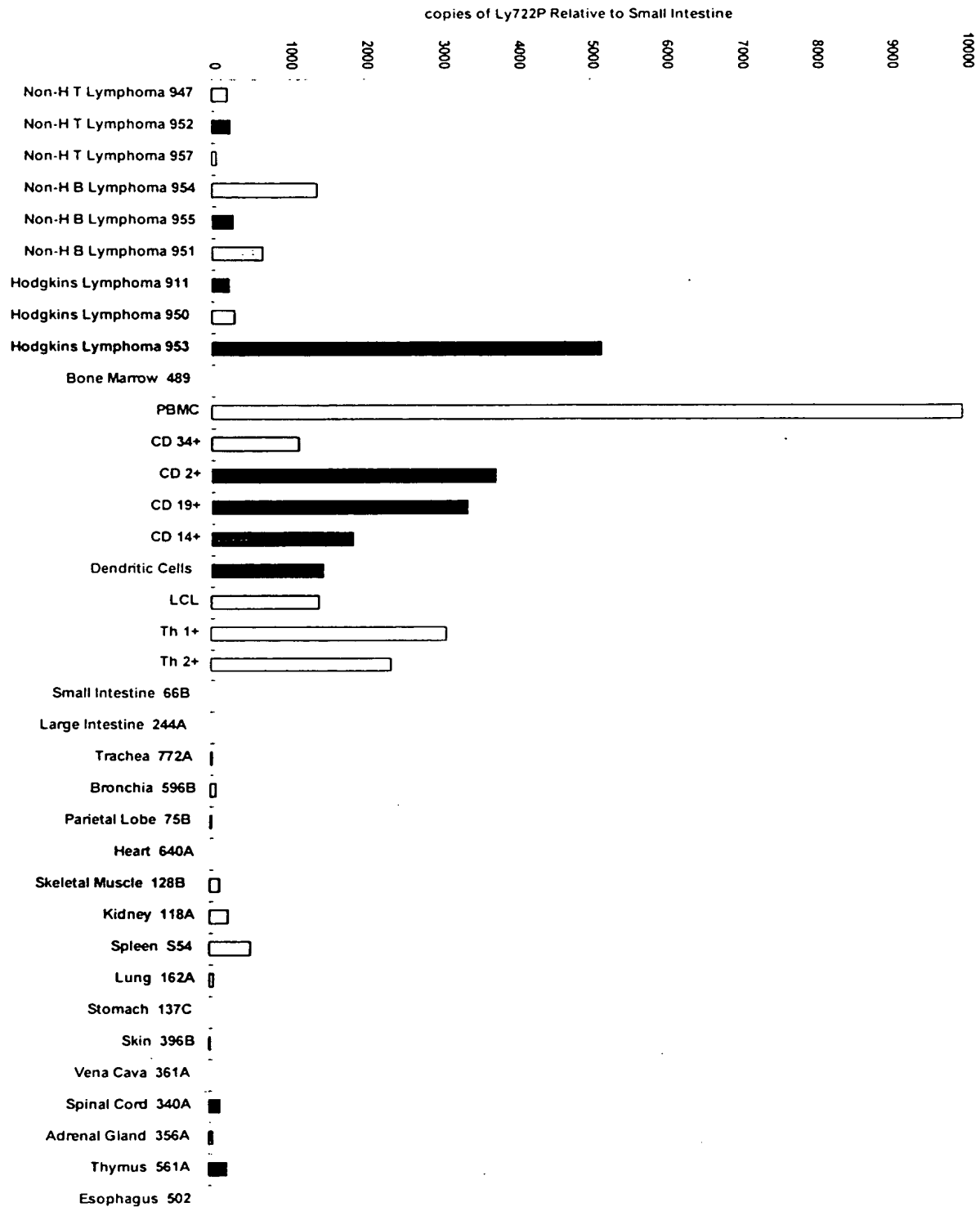


FIG. 4

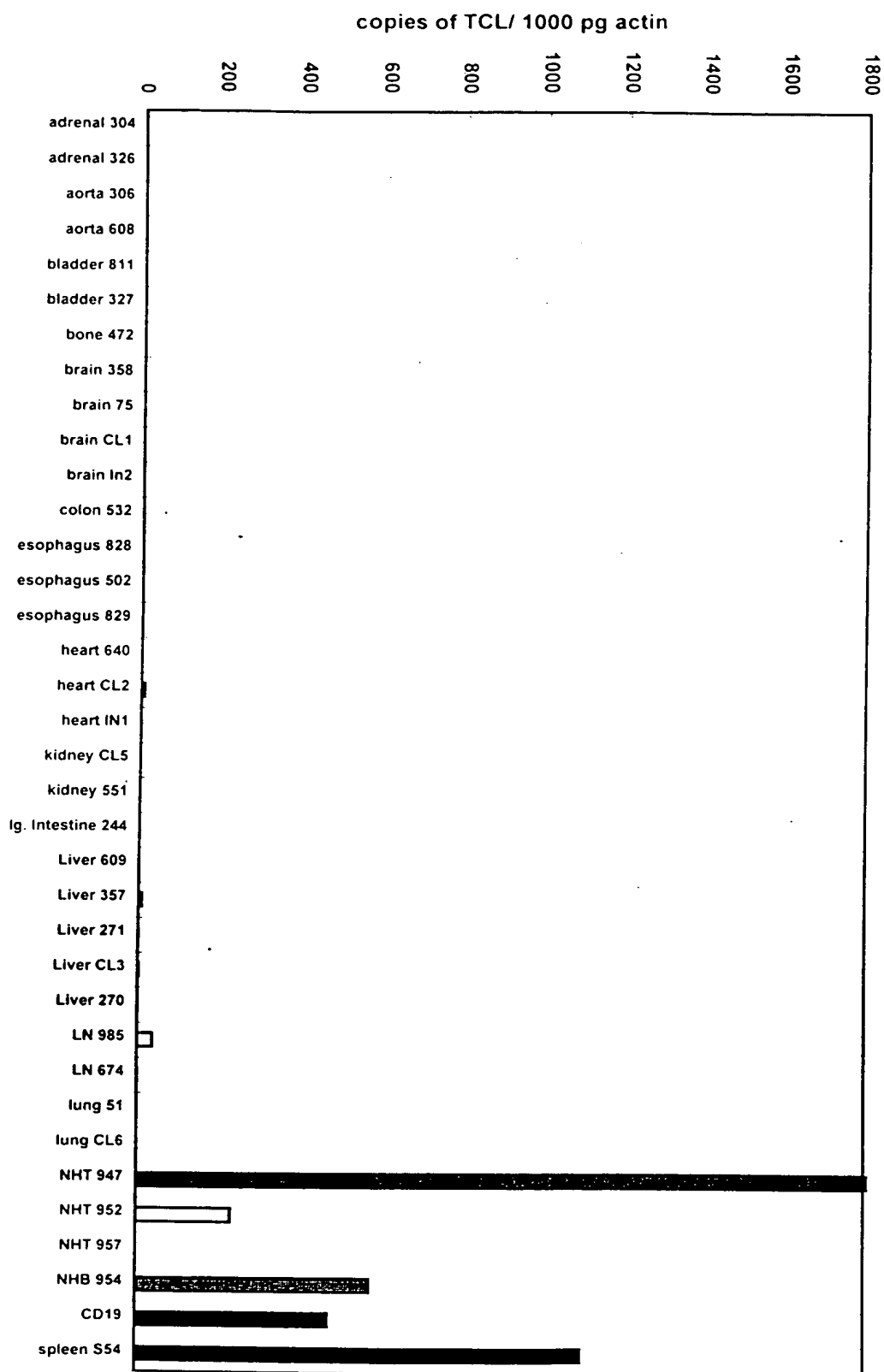
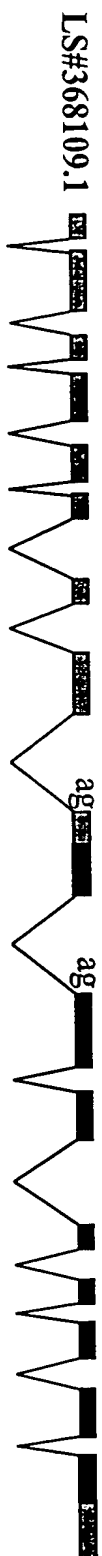
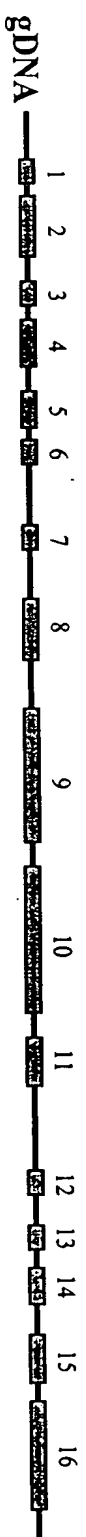


FIG. 5

# Chromosome 1:



LS#1384258.1

Ly1448P



SPAP1

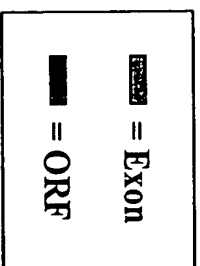
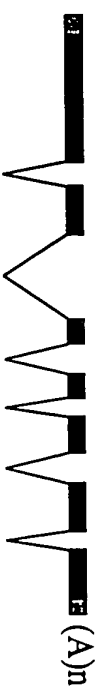


FIG. 6

A - AMPHI mid points of blocks.  
R - Residues matching the Rothbard/Taylor motif.  
D - Residues matching the IAd motif.  
d - Residues matching the IEd motif.

```

      5   10   15   20   25   30   35   40   45   50   55   60   65   70   75
MGKKTQRLSLSAELEIPAVKESDAGKYICRADNGHVPIQSKVVNIIPVRIPVSRPVLTLRSPGAQAAVGDLLLELHCE
.....AAAA.....AAAAA.....AAAAAAAAA.....RRRR.....DDDDDD.....DDDDDD.....
.....
      80   85   90   95  100  105  110  115  120  125  130  135  140  145  150
ALRGSPPILYQFYHEDVTLGNSSAPSGGGASFNLSTAEHSGNYSCEANNGLGAQCSEAVPVSISGPDGYRRDLM
.....AAAAA.AAA.....AAAAA.....RRR.....RRRR.....DDDDDD.....
.....
     155  160  165  170  175  180  185  190  195  200  205  210  215  220  225
TAGVLWGLFGVLGFTGVALLLYALFHKISGESSATNEPRGASRPNPQEFTYSSPTPDMEELQPVYVNVGSVDVDV
.....AAAAA.....AAAAA.....AAAAA.....RRRR.....RR.....DDDDDD.....DDDDDD.....DDD
R.RRRRRRRRRRRRR.....RRRR.....
.....
    230  235  240  245  250  255  260  265  270  275  280  285  290  295  300
VYSQVWSMQPESANIRTLLLENKDSQVIYSSVKKS
.....AAAAA.....
RRR.....RRRR.....
DDD.....
.....

```

FIG. 7



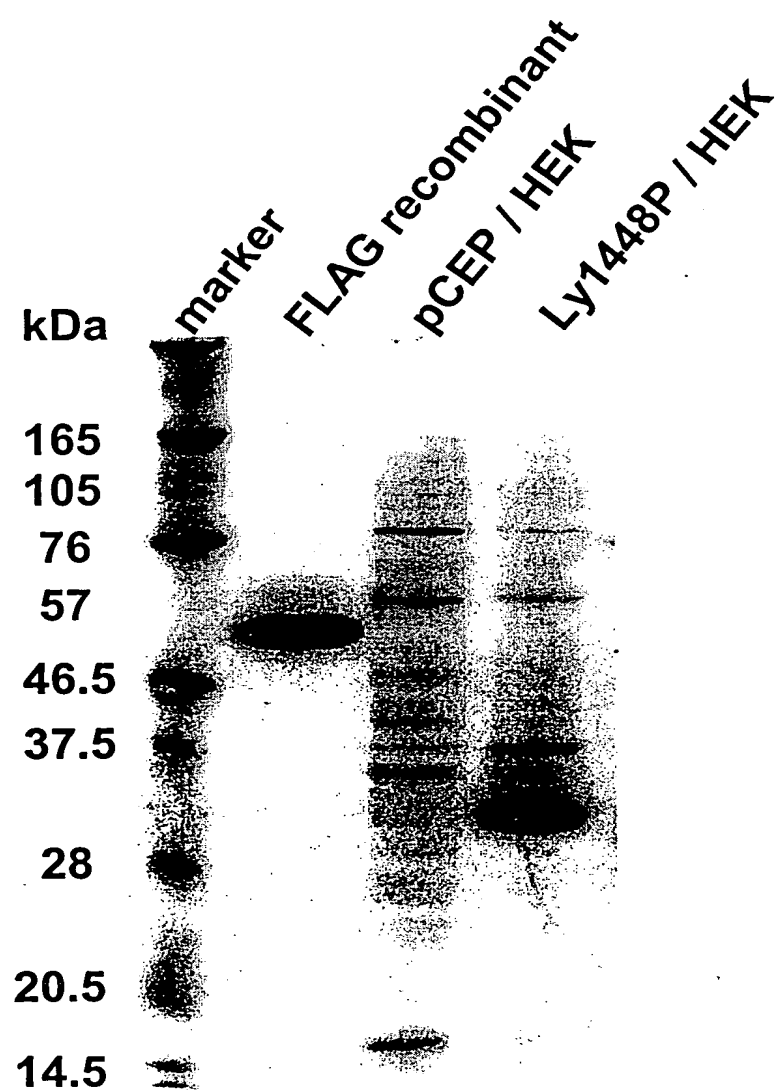


FIG. 8

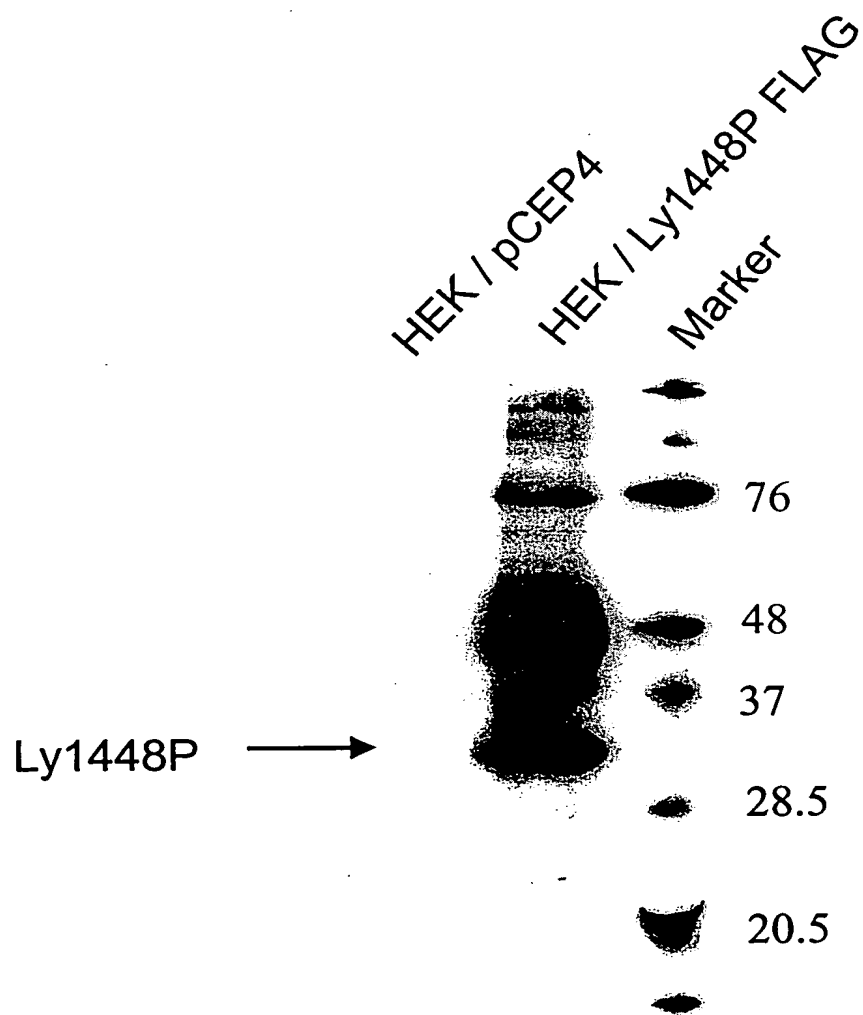


FIG. 9